GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: December 8, 2001, 19:13:06 ; Search time 2802.37 Seconds
(without alignments)
23323.767 Million cell updates/sec

Title: US-08-153-397A-1
Perfect score: 3962
Sequence: 1 CGGGCCTGAGACTGGGGTGA.....AAAAAAAAAAACCGGAATTC 3962

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
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3: gb_in:*
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31: em_htgo_inv:*
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33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3962	100.0	3962	6	I68738	I68738 Sequence 1
2	3625.6	91.5	3754	6	A42378	A42378 Sequence 1
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4	3613.4	91.2	3849	9	BC008716	BC008716 Homo sapi
5	3544.4	89.5	3803	9	HUMCAK	L20817 Homo sapien
6	3451	87.1	3637	6	AR094160	AR094160 Sequence
7	3451	87.1	3637	6	AR103004	AR103004 Sequence
8	3451	87.1	3637	6	AR105288	AR105288 Sequence
9	3451	87.1	3637	6	I80845	I80845 Sequence 3
10	3383.2	85.4	3554	9	HSTRKE	X74979 H.sapiens T
11	3366	85.0	3841	9	HSRETYK1	Z29093 H.sapiens E
12	3312.4	83.6	3692	9	HUMCAKA	L57508 Homo sapien
13	2405.6	60.7	3659	10	AF026259	AF026259 Mus muscu
14	2378.4	60.0	3674	10	MUSCAK	L57509 Mus musculu
15	2378	60.0	3743	10	RATPTK3D	L26525 Rattus norv
16	1192.2	30.1	1197	6	AR094162	AR094162 Sequence
17	1192.2	30.1	1197	6	AR103006	AR103006 Sequence
18	1192.2	30.1	1197	6	AR105290	AR105290 Sequence
19	1192.2	30.1	1197	6	I80847	I80847 Sequence 7
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c 22	1008.8	25.5	48731	9	AC004211	AC004211 Homo sapi
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24	950	24.0	12010	9	HSU48705	U48705 Human recep
25	642	16.2	3096	9	HSRPTK	X74764 H.sapiens m
26	642	16.2	3157	6	I68739	I68739 Sequence 3
c 27	642	16.2	3157	6	I68740	I68740 Sequence 5
28	639.8	16.1	3120	6	AR042425	AR042425 Sequence
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32	632.8	16.0	2521	10	AF329455	AF329455 Cricetulu
33	572	14.4	660	10	S77585	S77585 Ptk-3L=radi
34	394	9.9	400	11	G11190	G11190 SHGC-10808
35	362.4	9.1	200415	2	AC022301	AC022301 Mus muscu
c 36	362.4	9.1	203476	2	AC074150	AC074150 Mus muscu
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38	326.6	8.2	845	9	HSDRTK6	X99025 H.sapiens g
39	250.2	6.3	970	9	HSDRTK12	X99030 H.sapiens g
c 40	250	6.3	250	11	G15457	G15457 human STS S
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42	241.8	6.1	661	9	HSDRTK14	X99031 H.sapiens g
43	241.4	6.1	768	10	AF016247	AF016247 Rattus no
44	235	5.9	268	9	AF353182	AF353182 Homo sapi
45	234.6	5.9	1229	9	HSDRTK123	X98208 H.sapiens g

ALIGNMENTS

RESULT 1
I68738
LOCUS I68738 3962 bp DNA PAT 04-FEB-1998
DEFINITION Sequence 1 from patent US 5677144.
ACCESSION I68738
VERSION I68738.1 GI:2830860
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3962)
AUTHORS Ullrich,A. and Alves,F.HildegardElisabeth.
TITLE Recombinant DNA encoding CCK 2, a receptor tyrosine kinase
JOURNAL Patent: US 5677144-A 1 14-OCT-1997;
FEATURES Location/Qualifiers
source 1. .3962
/organism="unknown"
BASE COUNT 735 a 1234 c 1182 g 811 t
ORIGIN

Query Match 100.0%; Score 3962; DB 6; Length 3962;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3962; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy       1 CGGGCCTGAGACTGGGGTGACTGGGACCTAAGAGAATCCTGAGCTGGAGGCCCCCGACAG 60
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Db       1 CGGGCCTGAGACTGGGGTGACTGGGACCTAAGAGAATCCTGAGCTGGAGGCCCCCGACAG 60

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Qy     121 CCGGCTCCTGGCTCCCTCCGCCTCCCCCGCCCCTCGCCCCGCCGCCGAAGAGGCCCCGCT 180
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Qy     181 CCCGGGTCGGACGCCTGGGTCTGCCGGGAAGAGCGATGAGAGGTGTCTGAAGGTGGCTAT 240
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Qy     241 TCACTGAGCGATGGGGTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTA 300
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Qy     301 GGCCCGAGGGATCAGGAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCT 360
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Qy     421 CCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGT 480
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Qy     721 ACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGG 780
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Qy     961 CCTATGACGGACATACCGTGGGCGGACTGCAGTATGGGGGTCTGGGCCAGCTGGCAGATG 1020
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Qy    1021 GTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGGAGCTGCGGGTCTGGCCAGGCTATG 1080
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Qy    1081 ACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGT 1140
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Qy   2701 GCCGGAACCTCTATGCTGGGGACTATTACCGTGTGCAGGGCCGGGCAGTGCTGCCCATCC 2760
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Qy   3541 AGGAGAGGAAAATGTTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTC 3600
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A42378
LOCUS       A42378       3754 bp    DNA             PAT       06-MAR-1997
DEFINITION  Sequence 1 from Patent WO9502187.
ACCESSION   A42378
VERSION     A42378.1  GI:2297854
KEYWORDS    .
SOURCE      unidentified.
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REFERENCE   1  (bases 1 to 3754)
  AUTHORS   Gusterson,B.A., Crompton,M.R., Mitchell,P.J., Barker,K.T.,
            Martindale,J.E., Page,M.J. and Spence,P.
  TITLE     CELL GROWTH FACTOR RECEPTORS
  JOURNAL   Patent: WO 9502187-A 1 19-JAN-1995;
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COMMENT     Other publication AU 7081094 950206.
FEATURES             Location/Qualifiers
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BASE COUNT      712 a   1146 c   1121 g    775 t
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Qy    601 TCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGGGCCTGGGCAAGGAGT 660
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Qy    661 TCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGATGGTCGCCGCTGGATGGGCTGGAAGG 720
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Qy    721 ACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGG 780
Db    542 ACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGG 601

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Qy   1081 ACTATGTGGGATGGAGCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGT 1140
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Qy   1141 TTGACCGGCTGAGGGCCTTCCAGGCTATGCAGGTCCACTGTAACAACATGCACACGCTGG 1200
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Qy   1201 GAGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCCTGGG 1260
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Qy   1261 AGGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGGGGGACCCCAGAGCCCGGGCTG 1320
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Qy   1441 CGGCACTGGGAGGCACCTTCCCGCCAGCCCCCTGGTGGCCGCCTGGCCCACCTCCCACCA 1500
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Qy   1501 ACTTCAGCAGCTTGGAGCTGGAGCCCAGAGGCCAGC---AGCCCGTGGCCAAGGCCGAGG 1557
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Qy   1558 GGAGCCCGACCGCCATCCTCATCGGCTGCCTGGTGGCCATCATCCTGCTCCTGCTGCTCA 1617
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Qy   1618 TCATTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTCCTCAGCAAGGCTGAACGGA 1677
Db   1442 TCATTGCCCTCATGCTCTGGCGGCTGCACTGGCGCAGGCTCCTCAGCAAGGCTGAACGGA 1501

Qy   1678 GGGTGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCCCTGGGGACACTATCCTCATCA 1737
Db   1502 GGGTGTTGGAAGAGGAGCTGACGGTTCACCTCTCTGTCCCTGGGGACACTATCCTCATCA 1561

Qy   1738 ACAACCGCCCAGGTCCTAGAGAGCCACCCCCGTACCAGGAGCCCCGGCCTCGTGGGAATC 1797
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Qy   1798 CGCCCCACTCCGCTCCCTGTGTCCCCAATGGCTCTGCGTTGCTGCTCTCCAATCCAGCCT 1857
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Qy   1858 ACCGCCTCCTTCTGGCCACTTACGCCCGTCCCCCTCGAGGCCCGGGCCCCCCCACACCCG 1917
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Qy  1978 CAGGCGCCCCGCTTCTGCCCCCACCTCCCCAGAACAGCGTCCCCCATTATGCCGAGGCTG 2037
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Qy  2038 ACATTGTTACCCTGCAGGGCGTCACCGGGGGCAACACCTATGCTGTGCCTGCACTGCCCC 2097
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Qy  2158 AGGAGAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCACCTGTGTGAGGTCGACAGCCCTC 2217
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Qy  2218 AAGATCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTTGCTGGTAG 2277
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RESULT   3
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DEFINITION  Homo sapiens receptor tyrosine kinase mRNA, complete cds.
ACCESSION   L11315
VERSION     L11315.1  GI:403386
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KEYWORDS    receptor tyrosine kinase.
SOURCE      Homo sapiens (library: lambda-gt11) term placenta cDNA to mRNA.
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REFERENCE   1  (bases 1 to 3738)
  AUTHORS   Johnson,J.D., Edman,J.C. and Rutter,W.J.
  TITLE     A receptor tyrosine kinase found in breast carcinoma cells has an
            extracellular discoidin I-like domain
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681 (1993)
  MEDLINE   93296201
COMMENT     On Sep 27, 1993 this sequence version replaced gi:307397.
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ORIGIN
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Qy    421 CCCTGGGCATGCAGGACCGGACCATCCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGT 480
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Qy    481 CAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGGGATGGGGCCTGGT 540
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Db    302 CAGATTCCACTGCCGCCCGCCACAGCAGGTTGGAGAGCAGTGACGGGGATGGGGCCTGGT 361

Qy    541 GCCCCGCAGGGTCGGTGTTTCCCAAGGAGGAGGAGTACTTGCAGGTGGATCTACAACGAC 600
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Db    362 GCCCCGCAGGGTCGGTGTTTCCCAAGGAGGAGGAGTACTTGCAGGTGGATCTACAACGAG 421

Qy    601 TCCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGGGCCTGGGCAAGGAGT 660
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Qy  2461 ACCTCAACCAGTTCCTCAGTGCCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCTG 2520
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RESULT 4
BC008716
LOCUS BC008716 3849 bp mRNA PRI 12-JUL-2001
DEFINITION Homo sapiens, discoidin domain receptor family, member 1, clone MGC:8681 IMAGE:2964574, mRNA, complete cds.
ACCESSION BC008716
VERSION BC008716.1 GI:14250529
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3849)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R., Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 1 Row: o Column: 24
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 403386.

FEATURES Location/Qualifiers
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BASE COUNT 715 a 1181 c 1165 g 788 t
ORIGIN

Query Match 91.2%; Score 3613.4; DB 9; Length 3849;
Best Local Similarity 95.9%; Pred. No. 0;
Matches 3792; Conservative 0; Mismatches 31; Indels 130; Gaps 3;

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Qy     602 CCACCTGGTGGCTCTGGTGGGCACCCAGGGACGGCATGCCGGGGGCCTGGGCAAGGAGTT 661
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Qy     722 CCGCTGGGGTCAGGAGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGGA 781
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Qy    842 GAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGGATGGACTCCTGTCTTA 901
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Qy   1202 AGCCCGTCTGCCTGGCGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCCTGGGA 1261
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Qy   1262 GGGGGAGCCCATGCGCCACAACCTAGGGGGCAACCTGGGGGACCCCAGAGCCCGGGCTGT 1321
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Qy   1322 CTCAGTGCCCCTTGGCGGCCGTGTGGCTCGCTTTCTGCAGTGCCGCTTCCTCTTTGCGGG 1381
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Qy   1922 GGCCAAACCCACCAACACCCAGGCCTACAGTGGGGACTATATGGAGCCTGAGAAGCCAGG 1981
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Qy   2162 GAAGCTTGGCGAGGGCCAGTTTGGGGAGGTGCACCTGTGTGAGGTCGACAGCCCTCAAGA 2221
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Qy   2222 TCTGGTCAGTCTTGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTTGCTGGTAGCTGT 2281
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RESULT   5
HUMCAK
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DEFINITION  Homo sapiens tyrosine protein kinase (CAK) gene, complete cds.
ACCESSION   L20817
VERSION     L20817.1  GI:306474
KEYWORDS    A5-antigen; factor V; factor VIII; tyrosine protein kinase.
SOURCE      Homo sapiens fetus liver cDNA to mRNA.
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 3803)
  AUTHORS   Perez,J.L., Shen,X., Finkernagel,S., Sciorra,L., Jenkins,N.A.,
            Gilbert,D.J., Copeland,N.G. and Wong,T.W.
  TITLE     Identification and chromosomal mapping of a receptor tyrosine
            kinase with a putative phospholipid binding sequence in its
            ectodomain
  JOURNAL   Oncogene 9, 211-219 (1994)
  MEDLINE   94134417
REFERENCE   2  (bases 1 to 3803)
  AUTHORS   Johnson,J.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-FEB-1993) J.D. Johnson
REFERENCE   3  (sites)
  AUTHORS   Johnson,J.D., Edman,J.C. and Rutter,W.J.
  TITLE     A receptor tyrosine kinase found in breast carcinoma cells has an
            extracellular discoidin I-like domain
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681 (1993)
  MEDLINE   93296201
REFERENCE   4  (sites)
  AUTHORS   Wong,T.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JUL-1993) T. Wong
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BASE COUNT      721 a   1184 c   1123 g    775 t
ORIGIN

  Query Match           89.5%;  Score 3544.4;  DB 9;  Length 3803;
  Best Local Similarity  96.9%;  Pred. No. 0;
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Matches 3765; Conservative 0; Mismatches 21; Indels 98; Gaps 11;

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Qy      76 GCCTCCCGACACCCGAGCCCCGCCGGCGCCTCCCGCTCCCGGCTCCCG------GCTCCT 129
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Qy     850 GTCTGCGGGTAGAGCTCTATGGCTGCCTCTGGAGGGATGGACTCCTGTCTTACACCGCCC 909
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Qy     970 GACATACCGTGGGCGGACTGCAGTATGGGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGG 1029
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Qy    1150 TGAGGGCCTTCCAGGCTATGCAGGTCCACTGTAACAACATGCACACGCTGGGAGCCCGTC 1209
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Qy    1270 CCATGCGCCACAACCTAGGGGGCAACCTGGGGGACCCCAGAGCCCGGGCTGTCTCAGTGC 1329
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Qy    1390 TACTCTTCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTCCGGCACTGG 1449
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Qy    1570 CCATCCTCATCGGCTGCCTGGTGGCCATCATCCTGCTCCTGCTGCTCATCATTGCCCTCA 1629
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Qy   2230 GTCTTGATTTCCCCCTTAATGTGCGTAAGGGACACCCTTTGCTGGTAGCTGTCAAGATCT 2289
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Qy   2290 TACGGCCAGATGCCACCAAGAATGCCAGCTTCTCCTTGTTCTCCAGGAATGATTTCCTGA 2349
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Qy   2350 AAGAGGTGAAGATCATGTCGAGGCTCAAGGACCCCAACATCATTCGGCTGCTGGGCGTGT 2409
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RESULT 6
AR094160

LOCUS	AR094160 3637 bp DNA	PAT 08-SEP-2000
DEFINITION	Sequence 3 from patent US 6001621.	
ACCESSION	AR094160	
VERSION	AR094160.1 GI:10020905	
KEYWORDS	.	
SOURCE	Unknown.	
ORGANISM	Unknown.	
	Unclassified.	
REFERENCE	1 (bases 1 to 3637)	
AUTHORS	Godowski,P.J., Mark,M.R. and Scadden,D.T.	
TITLE	Protein tyrosine kinases	
JOURNAL	Patent: US 6001621-A 3 14-DEC-1999;	
FEATURES	Location/Qualifiers	
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ORIGIN		

Query Match 87.1%; Score 3451; DB 6; Length 3637;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3589; Conservative 0; Mismatches 5; Indels 105; Gaps 3;

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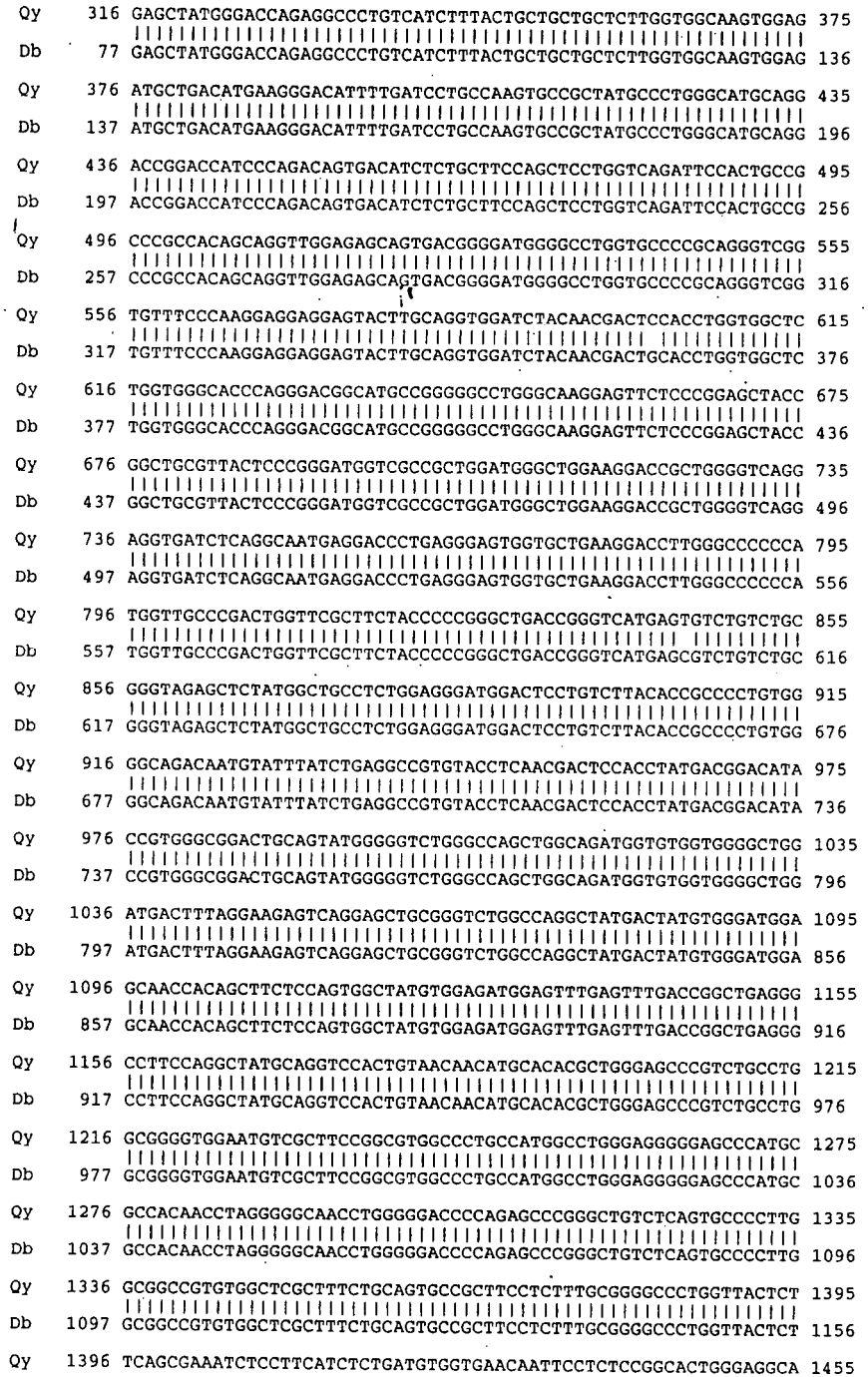
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Db 1937 GCCAGTTTGGGGAGGTGCACCTGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTCTTG 1996
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Db 2159 AGGACGACCCCCTCTGCATGATTACTGACTACATGGAGAACGGCGACCTCAACCAGTTCC 2218
Qy 2476 TCAGTGCCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGGCTG 2535

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Qy   2836 TGTGGGAGGTGCTGATGCTCTGTAGGGCCCAGCCCTTTGGGCAGCTCACCGACGAGCAGG 2895
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Qy   3196 AATAGAGGCAGTGAGACTGCAGGTGGGCTGGGCCCACCCAGGGAGCTGATGCCCCTTCTC 3255
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Qy   3256 CCCTTCCTGGACACACTCTCATGTCCCCTTCCTGTTCTTCCTTCCTAGAAGCCCCTGTCG 3315
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Qy   3495 ACACTGGACCCCACTGGCTGAGAATCTGGGGGTGAGGAGGACAAGAAGGAGAGGAAAATG 3554
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Qy   3555 TTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTCCTCCTCCATCACCT 3614
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Db   3213 TTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTCCTCCTCCATCACCT 3272

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Qy   3795 CACATTGATTTTTCTATAATCACTTGGGGTTTGTACATTTTTGGGGGGAGAGACACAGAT 3854
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DEFINITION  Sequence 3 from patent US 6087144.
ACCESSION   AR103004
VERSION     AR103004.1  GI:12814592
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 3637)
  AUTHORS   Scadden,D.T., Baker,K.P. and Baron,W.F.
  TITLE     Protein tyrosine kinases
  JOURNAL   Patent: US 6087144-A 3 11-JUL-2000;
FEATURES             Location/Qualifiers
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BASE COUNT      721 a   1094 c   1079 g    743 t
ORIGIN
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Query Match 87.1%; Score 3451; DB 6; Length 3637;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3589; Conservative 0; Mismatches 5; Indels 105; Gaps 3;

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Db     17 GTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTAGGCCCGAGGGATCAG 76

Qy    316 GAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCTTGGTGGCAAGTGGAG 375
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Db     77 GAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCTTGGTGGCAAGTGGAG 136

Qy    376 ATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATGCCCTGGGCATGCAGG 435
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Db    137 ATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATGCCCTGGGCATGCAGG 196

Qy    436 ACCGGACCATCCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGTCAGATTCCACTGCCG 495
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Qy    496 CCCGCCACAGCAGGTTGGAGAGCAGTGACGGGGATGGGGCCTGGTGCCCCGCAGGGTCGG 555
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Db    257 CCCGCCACAGCAGGTTGGAGAGCAGTGACGGGGATGGGGCCTGGTGCCCCGCAGGGTCGG 316

Qy    556 TGTTTCCCAAGGAGGAGGAGTACTTGCAGGTGGATCTACAACGACTCCACCTGGTGGCTC 615
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Db    317 TGTTTCCCAAGGAGGAGGAGTACTTGCAGGTGGATCTACAACGACTGCACCTGGTGGCTC 376

Qy    616 TGGTGGGCACCCAGGGACGGCATGCCGGGGGCCTGGGCAAGGAGTTCTCCCGGAGCTACC 675
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Qy    676 GGCTGCGTTACTCCCGGGATGGTCGCCGCTGGATGGGCTGGAAGGACCGCTGGGGTCAGG 735
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Qy    736 AGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGGACCTTGGGCCCCCCA 795
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Qy    976 CCGTGGGCGGACTGCAGTATGGGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGG 1035
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Qy   1036 ATGACTTTAGGAAGAGTCAGGAGCTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGA 1095
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Qy   1096 GCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGG 1155
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Db    857 GCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGG 916

Qy   1156 CCTTCCAGGCTATGCAGGTCCACTGTAACAACATGCACACGCTGGGAGCCCGTCTGCCTG 1215
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Db    917 CCTTCCAGGCTATGCAGGTCCACTGTAACAACATGCACACGCTGGGAGCCCGTCTGCCTG 976

Qy   1216 GCGGGGTGGAATGTCGCTTCCGGCGTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCATGC 1275
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Qy   1336 GCGGCCGTGTGGCTCGCTTTCTGCAGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTACTCT 1395
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Db    1097 GCGGCCGTGTGGCTCGCTTTCTGCAGTGCCGCTTCCTCTTTGCGGGGCCCTGGTTACTCT 1156

Qy   1396 TCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTCCGGCACTGGGAGGCA 1455
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Db    1157 TCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTCCGGCACTGGGAGGCA 1216

Qy   1456 CCTTCCCGCCAGCCCCCTGGTGGCCGCCTGGCCCACCTCCCACCAACTTCAGCAGCTTGG 1515
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Qy   2476 TCAGTGCCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGGCTG 2535
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Qy   3555 TTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTCCTCCTCCATCACCT 3614
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RESULT 8
AR105288
LOCUS AR105288 3637 bp DNA PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6096527.
ACCESSION AR105288
VERSION AR105288.1 GI:12818885
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 3637)
AUTHORS Godowski,P.J., Mark,M.R. and Scadden,D.T.
TITLE Nucleic acids encoding protein tryosine kinases
JOURNAL Patent: US 6096527-A 3 01-AUG-2000;
FEATURES Location/Qualifiers
source 1. .3637
/organism="unknown"
BASE COUNT 721 a 1094 c 1079 g 743 t
ORIGIN

Query Match 87.1%; Score 3451; DB 6; Length 3637;
Best Local Similarity 97.0%; Pred. No. 0;
Matches 3589; Conservative 0; Mismatches 5; Indels 105; Gaps 3;

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Qy    256 GTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTAGGCCCGAGGGATCAG 315
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Db     17 GTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTAGGCCCGAGGGATCAG 76

Qy    316 GAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCTTGGTGGCAAGTGGAG 375
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Db    137 ATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATGCCCTGGGCATGCAGG 196

Qy    436 ACCGGACCATCCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGTCAGATTCCACTGCCG 495
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Qy    976 CCGTGGGCGGACTGCAGTATGGGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGG 1035
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Db    797 ATGACTTTAGGAAGAGTCAGGAGCTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGA 856

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Qy   1396 TCAGCGAAATCTCCTTCATCTCTGATGTGGTGAACAATTCCTCTCCGGCACTGGGAGGCA 1455
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Db   2159 AGGACGACCCCCTCTGCATGATTACTGACTACATGGAGAACGGCGACCTCAACCAGTTCC 2218

Qy   2476 TCAGTGCCCACCAGCTGGAGGACAAGGCAGCCGAGGGGGCCCCTGGGGACGGGCAGGCTG 2535
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Db    3033 AAGGGTGGGGAGAAATATAGGATAGACACTGGACATGGCCCATTGGAGCACCTGGGCCCC 3092

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Db    3153 ACACTGGACCCCACTGGCTGAGAATCTGGGGGTGAGGAGGACAAGAAGGAGAGGAAAATG 3212

Qy    3555 TTTCCTTGTGCCTGCTCCTGTACTTGTCCTCAGCTTGGGCTTCTTCCTCCTCCATCACCT 3614
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RESULT   9
I80845
LOCUS       I80845       3637 bp    DNA             PAT       10-JUN-1998
DEFINITION  Sequence 3 from patent US 5709858.
ACCESSION   I80845
VERSION     I80845.1  GI:3209135
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.

REFERENCE   1  (bases 1 to 3637)
  AUTHORS   Godowski,P.J., Mark,M.R. and Scadden,D.T.
  TITLE     Antibodies specific for Rse receptor protein tyrosine kinase
  JOURNAL   Patent: US 5709858-A 3 20-JAN-1998;
FEATURES             Location/Qualifiers
     source          1. .3637
                     /organism="unknown"
BASE COUNT      721 a   1094 c   1079 g    743 t
ORIGIN


  Query Match             87.1%;  Score 3451;  DB 6;  Length 3637;
  Best Local Similarity   97.0%;  Pred. No. 0;
  Matches 3589;  Conservative    0;  Mismatches    5;  Indels  105;  Gaps    3;

Qy     256 GTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTAGGCCCGAGGGATCAG 315
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Db      17 GTTGGACTTGAAGGAATGCCAAGAGATGCTGCCCCCACCCCCTTAGGCCCGAGGGATCAG 76

Qy     316 GAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCTTGGTGGCAAGTGGAG 375
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Db      77 GAGCTATGGGACCAGAGGCCCTGTCATCTTTACTGCTGCTGCTCTTGGTGGCAAGTGGAG 136

Qy     376 ATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATGCCCTGGGCATGCAGG 435
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Db     137 ATGCTGACATGAAGGGACATTTTGATCCTGCCAAGTGCCGCTATGCCCTGGGCATGCAGG 196

Qy     436 ACCGGACCATCCCAGACAGTGACATCTCTGCTTCCAGCTCCTGGTCAGATTCCACTGCCG 495
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Qy     556 TGTTTCCCAAGGAGGAGGAGTACTTGCAGGTGGATCTACAACGACTCCACCTGGTGGCTC 615
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Qy     736 AGGTGATCTCAGGCAATGAGGACCCTGAGGGAGTGGTGCTGAAGGACCTTGGGCCCCCCA 795
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Qy    1036 ATGACTTTAGGAAGAGTCAGGAGCTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGA 1095
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Db    857 GCAACCACAGCTTCTCCAGTGGCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGG 916

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Qy   2176 GCCAGTTTGGGGAGGTGCACCTGTGTGAGGTCGACAGCCCTCAAGATCTGGTCAGTCTTG 2235
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Qy   2416 AGGACGACCCCCTCTGCATGATTACTGACTACATGGAGAACGGCGACCTCAACCAGTTCC 2475
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RESULT  10
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KEYWORDS    trk E gene; Trk E protein.
SOURCE      human.
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 3554)
  AUTHORS   Di Marco,E., Cutuli,N., Guerra,L., Cancedda,R. and De Luca,M.
  TITLE     Molecular cloning of trkE, a novel trk-related putative tyrosine
            kinase receptor isolated from normal human keratinocytes and widely
            expressed by normal human tissues
  JOURNAL   J. Biol. Chem. 268 (32), 24290-24295 (1993)
  MEDLINE   94043265
REFERENCE   2  (bases 1 to 3554)
  AUTHORS   De Luca,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-SEP-1993) M. De Luca, Istituto Nazionale per la
            Ricerca sul, Cancro, Lab Differenziamento Cellulare, Viale
            Benedetto XV, 10 - 16132 Genova, ITALY
FEATURES             Location/Qualifiers
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BASE COUNT      682 a   1064 c   1065 g    743 t
ORIGIN
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  Matches 3545;  Conservative    0;  Mismatches    3;  Indels  130;  Gaps    3;

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Qy    517 GCAGTGACGGGGATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGAGGAGGAGT 576
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Db    1558 ------------------------------------------------------------ 1557

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RESULT  11
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ACCESSION   Z29093
VERSION     Z29093.1  GI:732799
KEYWORDS    receptor tyrosine kinase.
SOURCE      human.
  ORGANISM  Homo sapiens
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REFERENCE   1  (bases 1 to 3841)
  AUTHORS   Laval,S., Butler,R., Shelling,A.N., Hanby,A.M., Poulsom,R. and
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  TITLE     Isolation and characterization of an epithelial-specific receptor
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  JOURNAL   Cell Growth Differ. 5 (11), 1173-1183 (1994)
  MEDLINE   95151638
REFERENCE   2  (bases 1 to 3841)
  AUTHORS   Shelling,A.N., Butler,R., Jones,T., Laval,S., Boyle,J.M. and
            Ganesan,T.S.
  TITLE     Localization of an epithelial-specific receptor kinase (EDDR1) to
            chromosome 6q16
  JOURNAL   Genomics 25 (2), 584-587 (1995)
  MEDLINE   95309932
REFERENCE   3  (bases 1 to 3841)
  AUTHORS   Kedinger,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1993) Claude Kedinger, CNRS Laboratoire de
            genetique moleculaire-U184, INSERM, 11, rue Humann, Strasbourg,
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     polyA_site      3828
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ORIGIN
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  Best Local Similarity   96.3%;  Pred. No. 0;
  Matches 3541;  Conservative    0;  Mismatches    5;  Indels  132;  Gaps    4;

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Db    953 AGGCCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACTGCAGTATG 1012
Qy    997 GGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGG 1056
Db   1013 GGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAAGAGTCAGG 1072
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RESULT 12
HUMCAKA

LOCUS	HUMCAKA	3692 bp	mRNA		PRI	31-JUL-1996

DEFINITION Homo sapiens Cak receptor kinase mRNA, complete cds.
ACCESSION L57508
VERSION L57508.1 GI:1160924
KEYWORDS receptor kinase.
SOURCE Homo sapiens lung cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3692)
AUTHORS Perez,J.L., Jing,S.Q. and Wong,T.W.
TITLE Identification of two isoforms of the Cak receptor kinase that are coexpressed in breast tumor cell lines
JOURNAL Oncogene 12 (7), 1469-1477 (1996)
MEDLINE 96204002
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BASE COUNT 704 a 1127 c 1102 g 759 t
ORIGIN

Query Match 83.6%; Score 3312.4; DB 9; Length 3692;
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SOURCE house mouse.
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AUTHORS Zerlin,M., Julius,M.A. and Goldfarb,M.
TITLE NEP: a novel receptor-like tyrosine kinase expressed in proliferating neuroepithelia
JOURNAL Oncogene 8 (10), 2731-2739 (1993)
MEDLINE 93390947
REFERENCE 2 (bases 1 to 3659)
AUTHORS Zerlin,M., Julius,M.A. and Goldfarb,M.

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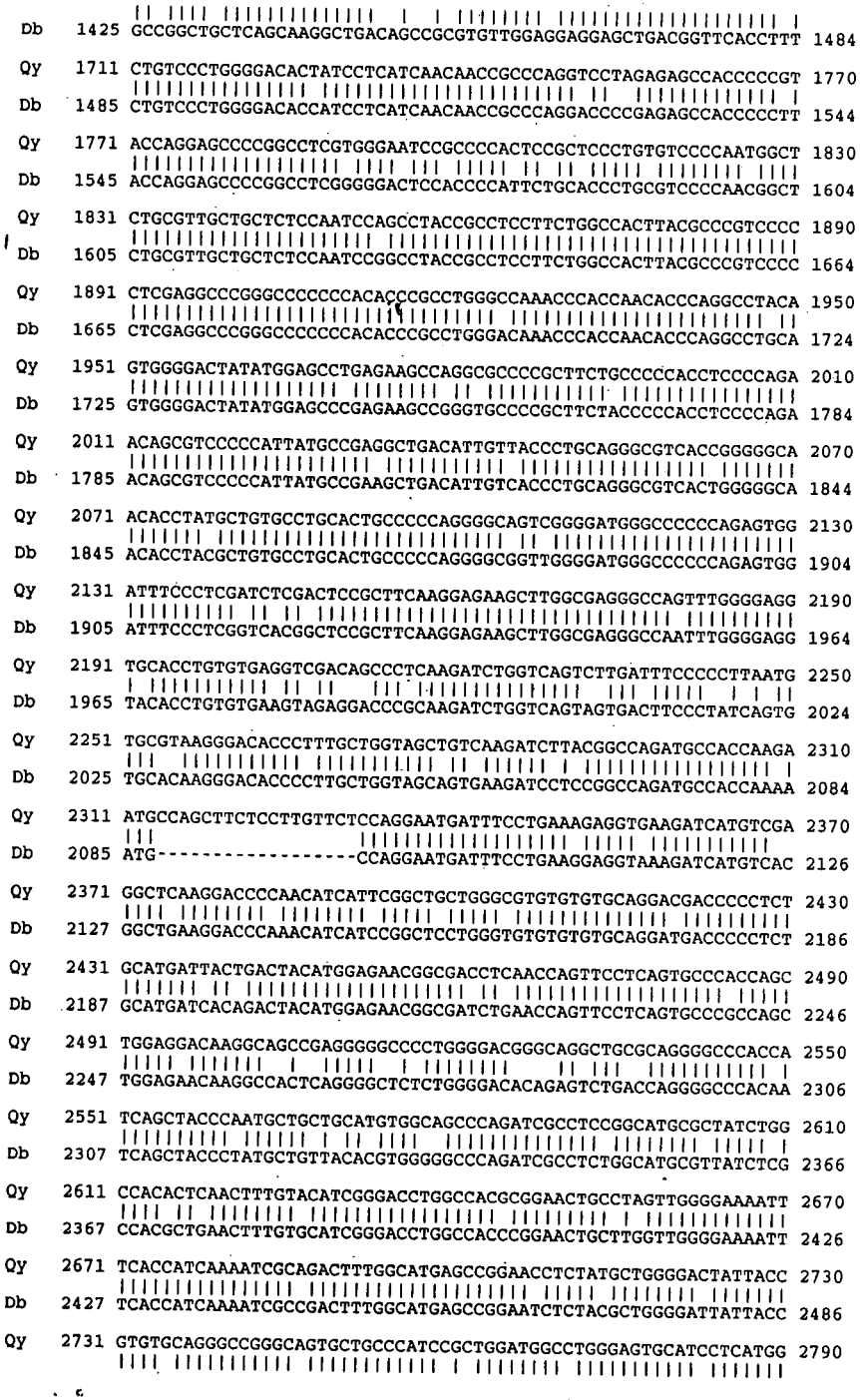
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Qy   3920 AAAGGTTGAGTTTT 3933
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Db   3607 AAAAGTTGAGTTGT 3620


RESULT  14
MUSCAK
LOCUS       MUSCAK       3674 bp    mRNA            ROD       31-JUL-1996
DEFINITION  Mus musculus Cak receptor kinase mRNA, complete cds.
ACCESSION   L57509
VERSION     L57509.1  GI:1161062
KEYWORDS    receptor kinase.
SOURCE      Mus musculus (strain C57BL) cDNA to mRNA.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 3674)
  AUTHORS   Perez,J.L., Jing,S.Q. and Wong,T.W.
  TITLE     Identification of two isoforms of the Cak receptor kinase that are
            coexpressed in breast tumor cell lines
  JOURNAL   Oncogene 12 (7), 1469-1477 (1996)
  MEDLINE   96204002
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ORIGIN


  Query Match           60.0%;  Score 2378.4;  DB 10;  Length 3674;
  Best Local Similarity  81.3%;  Pred. No. 0;
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Qy    277 AGAGATGCTGCCCCCACCCCCTTAGGCCCGAGGGATCAGGAGCTATGGGACCAGAGGCCC 336
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Db     63 AGAGATGCTGTCCCCTCCTCCATAGACCAGAGGGATCCAGAGCGATGGGGACAGGGACCC 122

Qy    337 TGTCATCTTTACTGCTGCTG---CTCTTGGTGGCAAGTGGAGATGCTGACATGAAGGGAC 393
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Db    123 TCTCATCTCTACTGCTGCTGCTACTCTTGGTGACAATTGGAGATGCTGACATGAAGGGAC 182

Qy    394 ATTTTGATCCTGCCAAGTGCCGCTATGCCCTGGGCATGCAGGACCGGACCATCCCAGACA 453
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Qy    454 GTGACATCTCTGCTTCCAGCTCCTGGTCAGATTCCACTGCCGCCCGCCACAGCAGGTTGG 513
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Db    243 GCGATATCTCTGTGTCCAGCTCCTGGTCGGACTCTACCGCTGCCCGCCACAGCAGGCTGG 302

Qy    514 AGAGCAGTGACGGGGATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGAGGAGG 573
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Db    303 AAAGCAGTGATGGAGATGGGGCTTGGTGCCCTGCAGGGCCTGTGTTCCCCAAAGAAGAGG 362

Qy    574 AGTACTTGCAGGTGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCAGGGAC 633
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Db    363 AGTACTTGCAGGTGGACCTTCGTAGGCTACACCTGGTGGCTCTGGTGGGCACCCAGGGAC 422

Qy    634 GGCATGCCCGGGGGCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGG 693
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Db    423 GCCATGCTGGGGGTCTGGGCAAAGAGTTCTCCCGAAGCTATCGGTTGCGTTACTCCCGAG 482

Qy    694 ATGGTCGCCGCTGGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGGCAATG 753
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Qy    754 AGGACCCTGAGGGAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACTGGTTC 813
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Db    543 AGGATCCCGGGGGAGTAGTGCTGAAGGACCTTGGGCCCCCCATGGTGGCCCGGCTGGTCC 602

Qy    814 GCTTCTACCCCCGGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCT 873
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Qy    874 GCCTCTGGAGGGATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTATTTAT 933
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Qy    934 CTGAGG---CCGTGTACCTCAACGACTCCACCTATGACGGACATACCGTGGGCGGACTGC 990
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Qy    991 AGTATGGGGGTCTGGGCCAGCTGGCAGATGGTGTGGTGGGGCTGGATGACTTTAGGAAGA 1050
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Db    783 AGTATGGCGGTCTGGGCCAGCTGGCAGATGGCGTGGTGGGCCTGGATGATTTCAGGCAGA 842

Qy   1051 GTCAGGAGCTGCGGGTCTGGCCAGGCTATGACTATGTGGGATGGAGCAACCACAGCTTCT 1110
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Qy   1111 CCAGTGGCTATGTGGAGATGGAGTTTGAGTTTGACCGGCTGAGGGCCTTCCAGGCTATGC 1170
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Qy   1171 AGGTCCACTGTAACAACATGCACACGCTGGGAGCCCGTCTGCCTGGCGGGGTGGAATGTC 1230
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Db    963 AGGTCCACTGTAACAACATGCACACTCTGGGAGCCCGCCTACCAGGTGGGGTGGAATGCC 1022

Qy   1231 GCTTCCGGCGTGGCCCTGCCATGGCCTGGGAGGGGGAGCCCATGCGCCACAACCTAGGGG 1290
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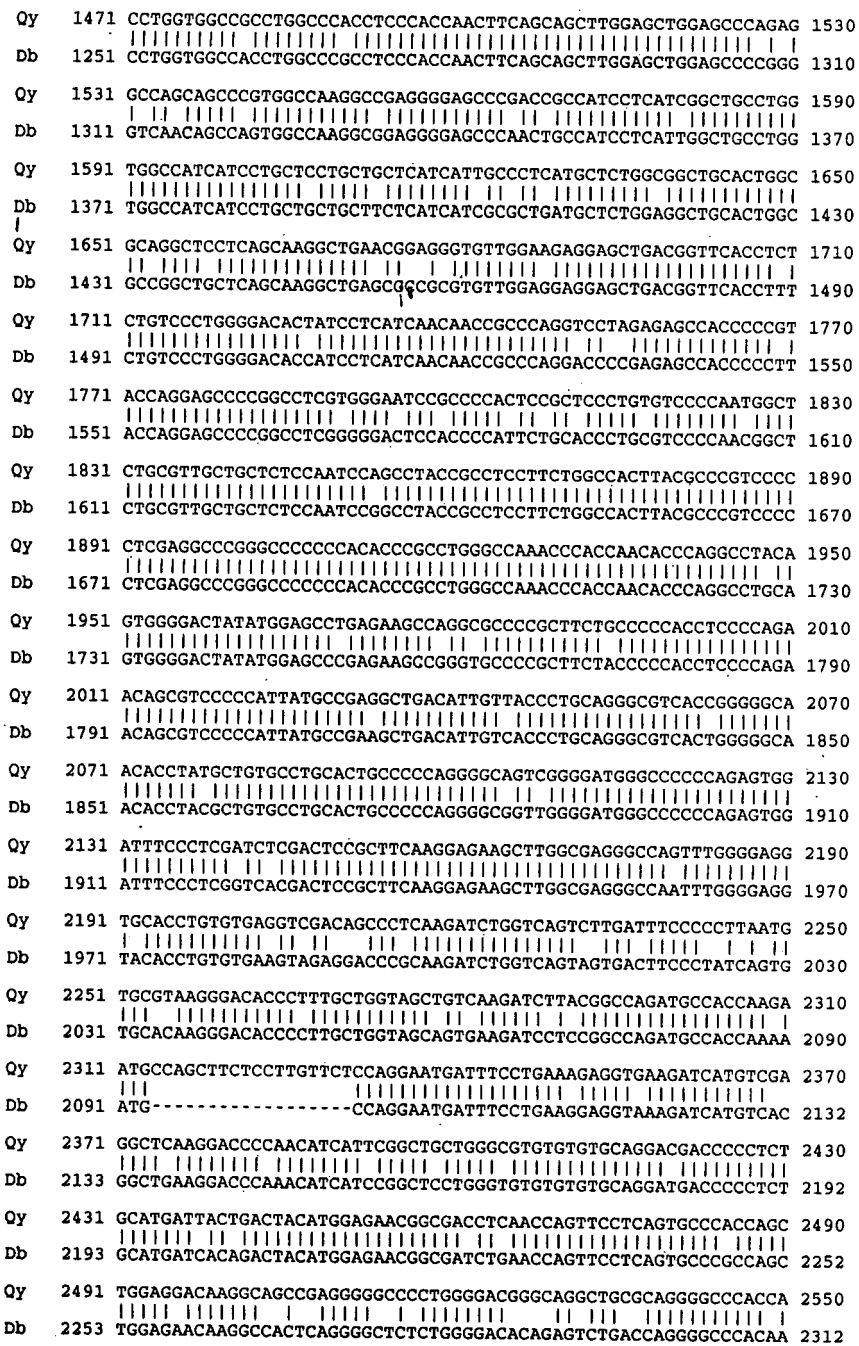

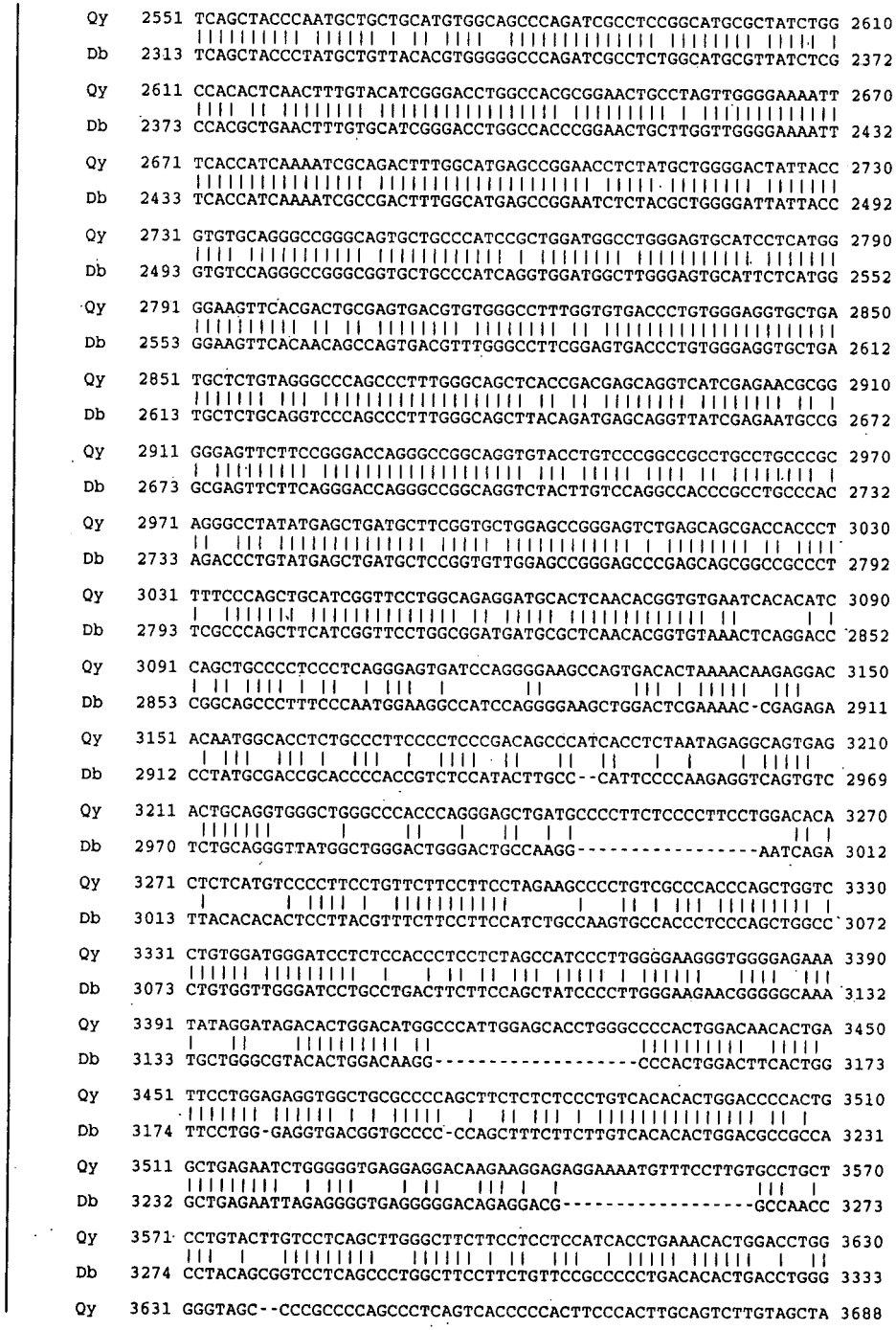

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Qy    3926 TGAGTT 3931

Db    3630 TGAGTT 3635


RESULT 15
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DEFINITION  Rattus norvegicus tyrosine kinase receptor (Ptk-3) gene, complete
            cds.
ACCESSION   L26525
VERSION     L26525.1  GI:432480
KEYWORDS    tyrosine kinase receptor.
SOURCE      Rattus norvegicus strain Sprague-Dawley DNA.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 3743)
  AUTHORS   Sanchez,M.P., Tapley,P., Saini,S.S., He,B., Pulido,D. and
            Barbacid,M.
  TITLE     Multiple tyrosine protein kinases in rat hippocampal neurons:
            isolation of Ptk-3, a receptor expressed in proliferative zones of
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  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 91 (5), 1819-1823 (1994)
  MEDLINE   94173920
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ORIGIN


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Db     195 CTCATCTCTCCTGCTGCTGCTACTCTTGGTGACAATTGGAGATGCTGACATGAAGGGACA 254

Qy     395 TTTTGATCCTGCCAAGTGCCGCTATGCCCTGGGCATGCAGGACCGGACCATCCCAGACAG 454

Db     255 TTTTGACCCAGCCAAGTGCCGCTATGCCCTGGGCATGCAGGACCGCACCATTCCAGACAG 314

Qy     455 TGACATCTCTGCTTCCAGCTCCTGGTCAGATTCCACTGCCGCCCGCCACAGCAGGTTGGA 514

Db     315 CGATATCTCTGTGTCCAGCTCCTGGTCGGACTCTACCGCCGCCCGCCACAGCAGGCTGGA 374

Qy     515 GAGCAGTGACGGGGATGGGGCCTGGTGCCCCGCAGGGTCGGTGTTTCCCAAGGAGGAGGA 574

Db     375 AAGCAGTGATGGAGATGGGGCTTGGTGCCCTGCAGGGCCTGTGTTCCCCAAAGAAGAGGA 434

Qy     575 GTACTTGCAGGTGGATCTACAACGACTCCACCTGGTGGCTCTGGTGGGCACCCAGGGACG 634

Db     435 GTACCTGCAGGTGGACCTTCGTAGGCTACACCTGGTGGCTCTGGTGGGCACCCAGGGCCG 494

Qy     635 GCATGCCGGGGGCCTGGGCAAGGAGTTCTCCCGGAGCTACCGGCTGCGTTACTCCCGGGA 694

Db     495 CCATGCTGGGGGTCTGGGCAAAGAGTTCTCCCGAAGCTACCGGTTGCGTTACTCCCGAGA 554

Qy     695 TGGTCGCCGCTGGATGGGCTGGAAGGACCGCTGGGGTCAGGAGGTGATCTCAGGCAATGA 754

Db     555 TGGCCGACGATGGATGGACTGGAAAGACAGATGGGGTCAGGAGGTGATTTCGGGTAACGA 614

Qy     755 GGACCCTGAGGGAGTGGTGCTGAAGGACCTTGGGCCCCCCATGGTTGCCCGACTGGTTCG 814

Db     615 GGATCCTGGGGGAGTGGTGCTGAAGGATCTCGGGCCCCCCATGGTGGCCCGGCTGGTCCG 674

Qy     815 CTTCTACCCCCGGGCTGACCGGGTCATGAGTGTCTGTCTGCGGGTAGAGCTCTATGGCTG 874

Db     675 TTTCTACCCCAGGGCTGACCGGGTCATGAGTGTCTGTCTTCGGGTGGAGCTCTATGGCTG 734

Qy     875 CCTCTGGAGGGATGGACTCCTGTCTTACACCGCCCCTGTGGGGCAGACAATGTATTTATC 934

Db     735 CCTCTGGCGGGACGGACTCTTGTCCTATACAGCCCCCGTGGGGCAGACCATGCAATTATC 794

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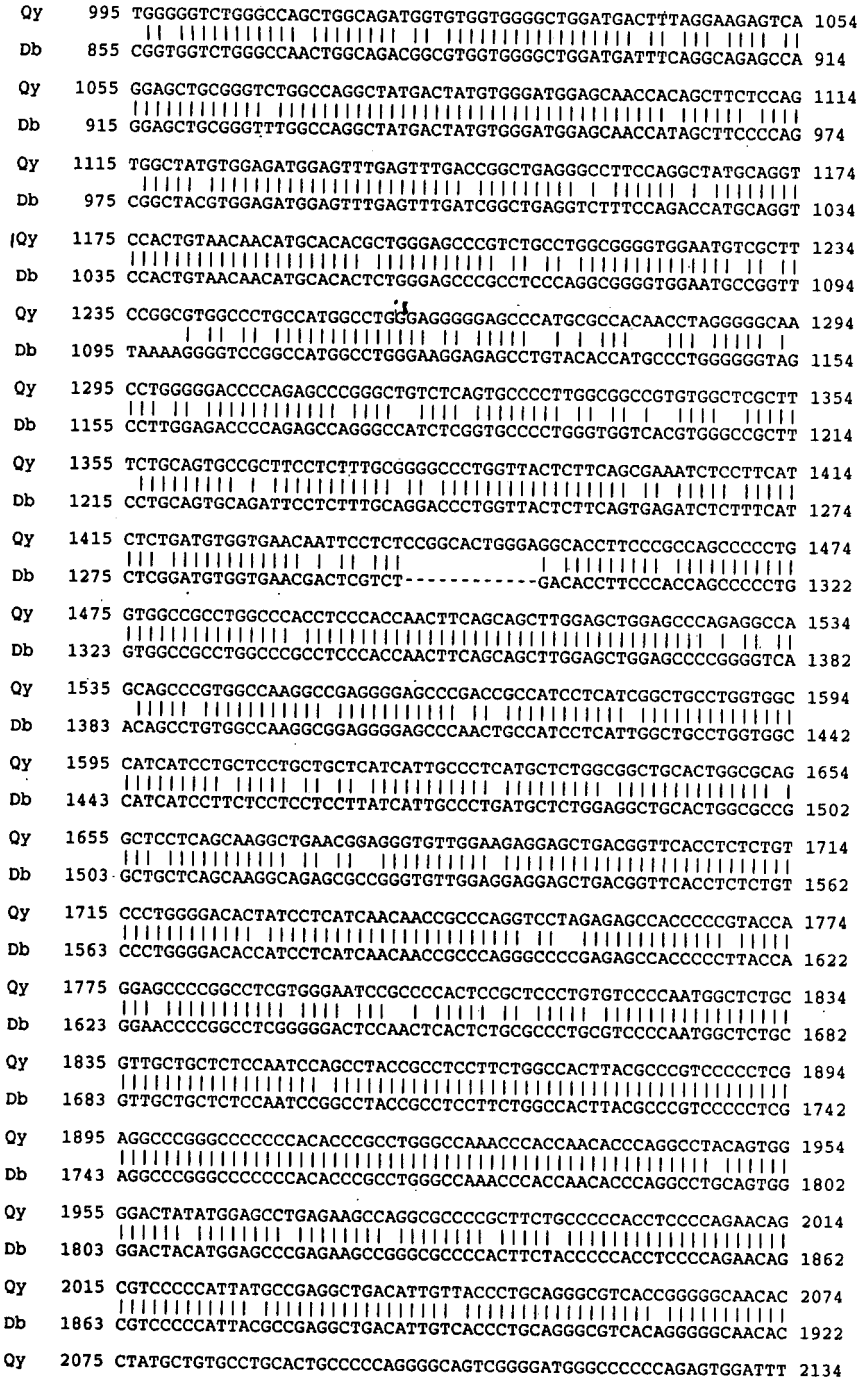
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